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ACCESS DB # 162299  
PLEASE PRINT CLEARLY

Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: DAVID GUZO Examiner #: 70677 Date: 8/11/05  
Art Unit: 1636 Phone Number: 2-0767 Serial Number: 10/695243  
Location (Bldg/Room#): 2A79 (Mailbox #): 2C70 Results Format Preferred (circle) PAPER DISK  
\*\*\*\*\*

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Date: \_\_\_\_\_

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please run a regular and interference sequence search  
on SEQ ID NO: 1 and 3.

1 Na 1389

3 Na 1389

Thanks

neg

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ACCESS DB # 163705  
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Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: DAVID GUZO Examiner #: 70677 Date: 8/24/05  
Art Unit: 1636 Phone Number: 2-0767 Serial Number: 10/695243  
Location (Bldg/Room#): Room 2A76 (Mailbox #): 2070 Results Format Preferred (circle): PAPER DISK  
\*\*\*\*\*

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: \_\_\_\_\_

Inventors (please provide full names): \_\_\_\_\_

Earliest Priority Date: \_\_\_\_\_

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

\*For Sequence Searches Only\* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search for nucleic acid sequences which  
encode a polypeptide at least 77%  
identical to SEQ ID NO:2 or 4.

Me

2 aa 462

4 aa 462

200 Hits } 1<sup>st</sup> pass  
50 align }

Therms

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 28, 2005, 14:09:22 ; Search time 730.5 Seconds  
(without alignment)  
3743.902 Million cells updates/sec

Title: US-10-695-243-4  
Perfect score: 2510  
Sequence: 1 MAKRRRTCTILSLFILF.....SEKSKEMTYALDQOQPAS 462

Scoring table:  
BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 200 summaries

Command line parameters:  
-MODE=frame+ p2n.model -DEV=x1h  
-O=/cgm2.1/USPTO.spool/US10695243/runat.26082005.123021.16577/app.query.fasta\_1.1294  
-DB=N Geneseg 16Dec04 -QWRT=fastcdp -SUPFIX=p2n.rng -MINMATCH=0.1 -LOOPC=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi  
-LIST=200 -DOCALIGN=200 -THR SCORE=Pct -THR MAX=100 -THR MIN=0 -ALIGN=50  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10695243@cgm2.1 1.957 @runat.26082005.123021.16577 -NCPU=6 -ICPU=3  
-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-BEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseg 16Dec04:\*  
1: geneseg19808:\*  
2: geneseg19908:\*  
3: geneseg20008:\*  
4: geneseg20018:\*  
5: geneseg20028:\*  
6: geneseg20038:\*  
7: geneseg20048:\*  
8: geneseg20058:\*  
9: geneseg20068:\*  
10: geneseg20078:\*  
11: geneseg20088:\*  
12: geneseg20098:\*  
13: geneseg20108:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	2510	100.0	1389	13 ADR46940 Mouse end
2	2176	86.7	3762	AD121896 Ad121896 Novel hum
3	2176	86.7	4386	5 ABV23530 Abv23530 Human pro
4	2176	86.7	4386	5 ABV29386 Abv29386 Human pro
5	2170	86.5	1389	13 ADR46938 ADR46938 Human liv

6	2118	84.4	4603	4 AAD08491 AAD08491 Human sec
7	1814	72.3	4320	8 ABA00835 ABA00835 Carboxydr
8	1777	70.8	2388	8 AAH17709 AAH17709 Human CDN
9	1469	58.5	2310	8 ABX70915 ABX70915 Novel hum
10	1414	56.3	1194	10 ADC26272 ADC26272 Human NOV
11	1259	50.2	2098	6 ABA05943 ABA05943 Human end
12	1247	49.7	2175	3 AAC79978 AAC79978 Human sec
13	1185	47.2	1840	12 ADO21136 ADO21136 Human car
14	948	37.8	2341	10 ADA53117 ADA53117 Human cod
15	795	31.7	1187	4 AAD08509 AAD08509 Human sec
16	741	29.5	713	5 ABA14746 ABA14746 Human pro
17	518	20.6	584	5 ABA44623 ABA44623 Human pro
18	518	20.6	584	5 ABA35823 ABA35823 Human pro
19	513	20.4	348	4 AAH06030 AAH06030 Human CDN
20	420.5	16.8	1380	4 ABL24141 ABL24141
21	390	15.5	550	12 ACH91730 ACH91730
22	366	14.6	3651	4 ABL24140 ABL24140
23	341	13.6	449	5 ABA05577 ABA05577
24	235	9.4	507	12 ACH78012 ACH78012
25	224.5	8.9	2297	10 ADE54765 ADE54765
26	214	8.5	920	6 ABA04209 ABA04209
27	214	8.5	920	6 ABA04208 ABA04208
28	193	7.7	920	6 ABA04207 ABA04207
29	193	7.7	920	6 ABA04206 ABA04206
30	141.5	5.6	2150	10 ADE54767 ADE54767
31	126	5.0	143	10 ACD95012 ACD95012
32	125.5	5.0	2794	4 ABL24142 ABL24142
33	119	4.7	2787	8 ACA24531 ACA24531
34	117	4.7	60	6 ABA35307 ABA35307
35	115	4.6	516	6 ABL37965 ABL37965
36	114.5	4.6	3081	8 ACA30982 ACA30982
37	113	4.5	2998	8 ABA59024 ABA59024
38	110	4.4	2037	6 ABL61255 ABL61255
39	110	4.4	2169	6 ABL61252 ABL61252
40	110	4.4	2235	6 ABL61256 ABL61256
41	110	4.4	2255	6 ABL61254 ABL61254
42	110	4.4	2367	6 ABL61253 ABL61253
43	110	4.4	2388	6 ABL61251 ABL61251
44	110	4.4	6419	6 ABA47189 ABA47189
45	108	4.3	1963	3 AAC47189 AAC47189
46	108	4.3	5917	6 ABA070972 ABA070972
47	107.5	4.3	228835	12 ADO97421 ADO97421
48	107	4.3	1434	6 ABA32546 ABA32546
49	107	4.3	8062	5 ABA82190 ABA82190
50	106.5	4.2	2678	8 ABA23469 ABA23469
51	106.5	4.2	4311	4 ABA62809 ABA62809
52	106.5	4.2	305107	4 ABA62809 ABA62809
53	104.5	4.2	2305	8 ABA89728 ABA89728
54	104.5	4.2	2661	10 ABA53839 ABA53839
55	104.5	4.2	4005	8 ABA14992 ABA14992
56	104.5	4.2	4008	6 ABA91416 ABA91416
57	104.5	4.2	4008	11 ABA02700 ABA02700
58	104.5	4.2	5299	11 ABA71342 ABA71342
59	104.5	4.2	5300	5 ABA62021 ABA62021
60	104.5	4.2	13715	6 ABA06152 ABA06152
61	104	4.1	1515	13 ABA45595 ABA45595
62	104	4.1	2385	8 ABA48172 ABA48172
63	104	4.1	3504	6 ABA66673 ABA66673
64	104	4.1	9240	13 ABA47281 ABA47281
65	103.5	4.1	1647	10 ABA70956 ABA70956
66	103.5	4.1	3955	2 ABA71317 ABA71317
67	103.5	4.1	4009	2 ABA71317 ABA71317
68	103.5	4.1	110000	10 ABA65388-07 ABA65388-07
69	103.5	4.1	110000	10 ABA65388-07 ABA65388-07
70	103	4.1	1740	8 ABA63458 ABA63458
71	103	4.1	1741	12 ABA084327 ABA084327
72	103	4.1	1741	13 ABA084327 ABA084327
73	103	4.1	1743	6 ABA97367 ABA97367
74	103	4.1	304905	11 ABA75180 ABA75180
75	102.5	4.1	1952	11 ABA03385 ABA03385
76	102.5	4.1	2259	3 ABA61154 ABA61154
77	102.5	4.1	2609	3 ABA61154 ABA61154
78	102.5	4.1	3313	3 ABA61144 ABA61144
				AAD08491 Human sec
				ABA00835 Carboxydr
				AAH17709 Human CDN
				ABX70915 Novel hum
				ADC26272 Human NOV
				ABA05943 Human end
				AAC79978 Human sec
				ADO21136 Human car
				ADA53117 Human cod
				AAD08509 Human sec
				ABA14746 Human pro
				ABA44623 Human pro
				ABA35823 Human pro
				AAH06030 Human CDN
				ABL24141 Drosophil
				ACH91730 Human gen
				ABL24140 Drosophil
				ABA05577 Human pro
				ACH78012 Human gen
				ADE54765 Rat gene
				ABA04209 Oligonuc1
				ABA04208 Oligonuc1
				ABA04207 Oligonuc1
				ABA04206 Oligonuc1
				ABA59024 Prunus se
				ABA161255 S. mutans
				ABA161252 S. mutans
				ABA161256 S. mutans
				ABA161254 S. mutans
				ABA161253 S. mutans
				ABA161251 S. mutans
				ABA47189 Human jmm
				ABA70972 Listeria
				ABA32546 Candida a
				ABA82190 DNA. encod
				ABA23469 Coding se
				ABA62809 Shrimp wh
				ABA89728 Shrimp wh
				ABA53839 Primary r
				ABA14992 Pathogen
				ABA91416 Staphyloc
				ABA02700 Staphyloc
				ABA71342 DNA seque
				ABA62021 E. canis
				ABA06152 MUC5B par
				ABA45595 Bacterial
				ABA48172 Prokaryot
				ABA66673 Streptococ
				ABA47281 Bacterial
				ABA70956 Photocorab
				ABA71317 Complete
				ABA71317 Complete
				ABA65388-07 Continuation (41 o
				ABA65388-07 Continuation (8 of
				ABA63458 Human CDN
				ABA084327 Tumour-as
				ABA97367 Gene #386
				ABA75180 Human Bnd
				ABA03385 Human CDN
				ABA61154 SEN virus
				ABA61154 SEN virus
				ABA61144 SEN virus

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus.p2n model

Run on: August 28, 2005, 14:11:42 ; Search time 6175.5 Seconds  
(without alignments)  
3625.020 Million cell updates/sec

Title: US-10-695-243-2  
Perfect score: 2501  
Sequence: 1 MAKFRRRRTCTIILALFILFIF.....SEKYSKERATYALDRQLPVS 462

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues  
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 200 summaries

Command line parameters:

-MODEL=frame.p2n.model -DEV=xlh  
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-DB=genemb1 -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blomsu62 -TRANS=human40.cdi -LIST=200  
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=50 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MUTLEN=0 -MAXLEN=2000000000  
-USER=US10695243 @CGCN 1.1 7837 @runat\_26082005\_123021\_16586 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmb1:  
1: gb\_ba:\*  
2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_scs:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2501	100.0	1389	6	CQ868818 Sequence
2	2501	100.0	4596	9	BSM806986
3	2497	99.8	4386	6	CQ491652 Sequence
4	2497	99.8	4386	6	CQ497537 Sequence

5	2492	99.6	1474	9	BSA577574
6	2490	99.6	4558	9	BSM806565
7	2180	87.2	4455	10	BC067076
8	2170	86.8	1389	6	CQ868820
9	1972	78.8	2552	10	AF023657
10	1962	78.4	2388	6	BD159701
11	1962	78.4	2388	6	AX882397 Sequence
12	1962	78.4	2388	6	AK022900
13	1639	67.9	2779	5	BC077304
14	1639	66.7	1408	5	CR354351
15	1458.5	58.3	2770	10	BC065047
16	1447	57.9	2310	6	AR541894
17	1401	56.0	1083	6	C0722353
18	1305.5	52.2	123789	2	AC110674
19	1199.5	48.0	3286	5	BC081681
20	1178	47.1	1859	9	BC063587
21	1176	47.0	105273	9	AL671884
22	1093	43.7	782	9	AY048774
23	1077	43.1	256771	2	AC115326
24	1058	42.3	193704	10	AL805949
25	1006	40.2	2120	9	BC077730
26	1006	40.2	2338	9	AB188490
27	985	39.4	1096	9	AY048775
28	949	37.9	2241	6	AX714001
29	949	37.9	2341	9	AK055996
30	898	35.9	713	6	CQ482870
31	852	34.1	181070	2	AC142187
32	851	34.0	301630	1	AB016942
33	845	33.8	134161	9	AC104336
34	845	33.8	143060	9	AL929472
35	845	33.8	170908	2	AC022557
36	845	33.8	190310	2	AC023225
37	845	33.8	255952	2	AL513473
38	842.5	33.7	177067	2	AC016516
39	841.5	33.6	58345	9	AC011999
40	835	33.4	197552	10	AL606933
41	702	28.1	781	6	C0722373
42	664	26.5	584	6	CQ030374
43	664	26.5	584	6	CQ512775
44	662	26.5	1347	9	BC009952
45	587	22.8	1246	5	BC930133
46	589	22.8	67717	2	AC101393
47	553	22.1	348	6	BD148022
48	553	22.1	348	6	AX867960
49	535.5	21.4	1075	9	BC038190
50	519	20.8	797	11	BV174680
51	504	20.2	1357	9	BC031903
52	467	18.7	449	6	CQ473701
53	415	16.6	2136	3	AY071523
54	395	15.8	1380	6	CQ005694
55	389	15.6	190310	2	AC023225
56	348	13.9	44117	2	AC017312
57	346	13.8	3651	6	CQ056593
58	346	13.8	164884	3	AC011063
59	346	13.8	193924	3	AC009910
60	346	13.8	260249	3	AE003610
61	262	10.5	673	6	AR508592
62	246	9.8	622	11	BV022021
63	188.5	7.5	347800	1	AP000060
64	178.5	7.1	685	9	BSA33442
65	178	7.1	600	9	BSA334516
66	176.5	7.1	861	9	BSA334462
67	170	6.8	826	9	BSA330260
68	170	6.8	753	9	BSA336605
69	149.5	6.0	167000	1	AP000059
70	146.5	5.9	300254	1	AB016933
71	140	5.6	236120	14	AP063866
72	138	5.5	516	6	AX341307
73	135.5	5.4	349980	6	AX344557
74	130	5.2	10317	1	AB005739
75	126	5.0	10317	6	CQ538420
76	125.5	5.0	169546	2	AC004157
77	125.5	5.0	302605	1	AB016938